

GG	GCG	CGA	GCG	CCT	CAG	CGC	GGC	CGC	TCG	CTC	TCC	CCC	38
	Ala	Arg	Ala	Pro	Gln	Arg	Gly	Arg	Ser	Leu	Ser	Pro	
	1				5					10			
TCG	AGG	GAC	AAA	CTT	TTC	CCA	AAC	CCG	ATC	CGA	GCC	CTT	77
Ser	Arg	Asp	Lys	Leu	Phe	Pro	Asn	Pro	Ile	Arg	Ala	Leu	
		15					20					25	
GGA	CCA	AAC	TCG	CCT	GCG	CCG	AGA	GCC	GTC	CGC	GTA	GAG	116
Gly	Pro	Asn	Ser	Pro	Ala	Pro	Arg	Ala	Val	Arg	Val	Glu	
				30					35				
CGC	TCC	GTC	TCC	GGC	GAG	ATG	TCC	GAG	CGC	AAA	GAA	GGC	155
Arg	Ser	Val	Ser	Gly	Glu	Met	Ser	Glu	Arg	Lys	Glu	Gly	
	40					45					50		
AGA	GGC	AAA	GGG	AAG	GGC	AAG	AAG	AAG	GAG	CGA	GGC	TCC	194
Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Glu	Arg	Gly	Ser	
			55					60					
GGC	AAG	AAG	CCG	GAG	TCC	GCG	GCG	GGC	AGC	CAG	AGC	CCA	233
Gly	Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	
	65				70					75			
GCC	TTG	CCT	CCC	CGA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	272
Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	
		80					85					90	
TCG	GCT	GCA	GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	311
Ser	Ala	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	
				95					100				
AGT	TCT	GAA	TAC	TCC	TCT	CTC	AGA	TTC	AAG	TGG	TTC	AAG	350
Ser	Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	
	105					110					115		
AAT	GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC	AAA	CCA	CAA	AAT	389
Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	Pro	Gln	Asn	
			120					125					
ATC	AAG	ATA	CAA	AAA	AAG	CCA	GGG	AAG	TCA	GAA	CTT	CGC	428
Ile	Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	
	130				135					140			
ATT	AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA	GAG	TAT	ATG	467
Ile	Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	
		145					150					155	
TGC	AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	506
Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	
				160					165				

FIG. 1A

GCC AAT ATC ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT 545
 Ala Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr
 170 175 180

GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA 584
 Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser
 185 190

GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA 623
 Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
 195 200 205

AAT ACT TCT TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA 662
 Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 210 215 220

AGC CAT CTT GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC 701
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe
 225 230

TGT GTG AAT GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT 740
 Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu
 235 240 245

TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC CAA CCT GGA 779
 Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Gln Pro Gly
 250 255

TTC ACT GGA GCA AGA TGT ACT GAG AAT GTG CCC ATG AAA 818
 Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
 260 265 270

GTC CAA AAC CAA GAA AAG GCG GAG GAG CTG TAC CAG AAG 857
 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys
 275 280 285

AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC GCC CTC CTT 896
 Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu
 290 295

GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC TGC AAA ACC 935
 Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr
 300 305 310

AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT CTT CGG CAG 974
 Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln
 315 320

AGC CTT CGG TCT GAA CGA AAC AAT ATG ATG AAC ATT GCC 1013
 Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile Ala
 325 330 335

FIG. 1B

AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	CCC	GAG	AAT	GTC	1052
Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	Pro	Glu	Asn	Val	
		340					345					350	
CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	AAC	GTC	ATC	TCC	1091
Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn	Val	Ile	Ser	
			355						360				
AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG	ACA	TCC	TTT	1130
Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	Thr	Ser	Phe	
	365					370					375		
TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	CAC	TCC	ACT	1169
Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr	
			380					385					
ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	AGC	AAC	GGA	1208
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	
	390				395					400			
CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	CAC	TCT	GTA	ATC	1247
His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	His	Ser	Val	Ile	
		405					410					415	
GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	CAC	AGC	AGC	CCA	1286
Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	His	Ser	Ser	Pro	
				420						425			
ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	GGC	ACA	GGA	GGC	1325
Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	Thr	Gly	Gly	
	430					435					440		
CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	GAA	1364
Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	Glu	
			445					450					
ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AGG	1403
Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser	Glu	Arg	
	455				460					465			
TAT	GTG	TCA	GCC	ATG	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	1442
Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	
		470					475					480	
GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAA	TCG	CCC	CCT	1481
Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	
			485						490				
TCG	GAA	ATG	TCT	CCA	CCC	GTG	TCC	AGC	ATG	ACG	GTG	TCC	1520
Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	Met	Thr	Val	Ser	
	495					500					505		

FIG. 1C

ATG CCT TCC ATG GCG GTC AGC CCC TTC ATG GAA GAA GAG 1559
 Met Pro Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu
 510 515

AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG CGG GAG 1598
 Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu
 520 525 530

AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC 1637
 Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe
 535 540 545

CAC CAC AAC CCC GCG CAT GAC AGT AAC AGC CTC CCT GCT 1676
 His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala
 550 555

AGC CCC TTG AGG ATA GTG GAG GAT GAG GAG TAT GAA ACG 1715
 Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr
 560 565 570

ACC CAA GAG TAC GAG CCA GCC CAA GAG CCT GTT AAG AAA 1754
 Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys
 575 580

CTC GCC AAT AGC CGG CGG GCC AAA AGA ACC AAG CCC AAT 1793
 Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn
 585 590 595

GGC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC ACA 1832
 Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser Asn Thr
 600 605 610

AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT 1871
 Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp
 615 620

GAA AGA GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG 1910
 Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln
 625 630 635

AAC CCC CTG GCA GCC AGT CTT GAG GCA ACA CCT GCC TTC 1949
 Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe
 640 645

CGC CTG GCT GAC AGC AGG ACT AAC CCA GCA GGC CGC TTC 1988
 Arg Leu Ala Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe
 650 655 660

TCG ACA CAG GAA GAA ATC CAG G 2010
 Ser Thr Gln Glu Glu Ile Gln
 665 669

FIG. 1D

GG	GAC	AAA	CTT	TTC	CCA	AAC	CCG	ATC	CGA	GCC	CTT	GGA	38
	Asp	Lys	Leu	Phe	Pro	Asn	Pro	Ile	Arg	Ala	Leu	Gly	
	1				5					10			
CCA	AAC	TCG	CCT	GCG	CCG	AGA	GCC	GTC	CGC	GTA	GAG	CGC	77
Pro	Asn	Ser	Pro	Ala	Pro	Arg	Ala	Val	Arg	Val	Glu	Arg	
		15					20					25	
TCC	GTC	TCC	GGC	GAG	ATG	TCC	GAG	CGC	AAA	GAA	GGC	AGA	116
Ser	Val	Ser	Gly	Glu	Met	Ser	Glu	Arg	Lys	Glu	Gly	Arg	
				30					35				
GGC	AAA	GGG	AAG	GGC	AAG	AAG	AAG	GAG	CGA	GGC	TCC	GGC	155
Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	Glu	Arg	Gly	Ser	Gly	
	40					45					50		
AAG	AAG	CCG	GAG	TCC	GCG	GCG	GGC	AGC	CAG	AGC	CCA	GCC	194
Lys	Lys	Pro	Glu	Ser	Ala	Ala	Gly	Ser	Gln	Ser	Pro	Ala	
			55					60					
TTG	CCT	CCC	CAA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	TCG	233
Leu	Pro	Pro	Gln	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	
	65				70					75			
GCT	GCA	GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	AGT	272
Ala	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	
		80					85					90	
TCT	GAA	TAC	TCC	TCT	CTC	AGA	TTC	AAG	TGG	TTC	AAG	AAT	311
Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	Asn	
				95					100				
GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC	AAA	CCA	CAA	AAT	ATC	350
Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	Pro	Gln	Asn	Ile	
	105					110					115		
AAG	ATA	CAA	AAA	AAG	CCA	GGG	AAG	TCA	GAA	CTT	CGC	ATT	389
Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	Ile	
			120					125					
AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA	GAG	TAT	ATG	TGC	428
Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys	
	130				135					140			
AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	467
Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	
		145					150					155	
AAT	ATC	ACC	ATC	GTG	GAA	TCA	AAC	GAG	ATC	ATC	ACT	GGT	506
Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Glu	Ile	Ile	Thr	Gly	
				160					165				

FIG. 2A

ATG	CCA	GCC	TCA	ACT	GAA	GGA	GCA	TAT	GTG	TCT	TCA	GAG	545
Met	Pro	Ala	Ser	Thr	Glu	Gly	Ala	Tyr	Val	Ser	Ser	Glu	
	170					175					180		
TCT	CCC	ATT	AGA	ATA	TCA	GTA	TCC	ACA	GAA	GGA	GCA	AAT	584
Ser	Pro	Ile	Arg	Ile	Ser	Val	Ser	Thr	Glu	Gly	Ala	Asn	
			185					190					
ACT	TCT	TCA	TCT	ACA	TCT	ACA	TCC	ACC	ACT	GGG	ACA	AGC	623
Thr	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Gly	Thr	Ser	
195					200					205			
CAT	CTT	GTA	AAA	TGT	GCG	GAG	AAG	GAG	AAA	ACT	TTC	TGT	662
His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	
		210					215					220	
GTG	AAT	GGA	GGG	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	701
Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	
				225					230				
AAC	CCC	TCG	AGA	TAC	TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	740
Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	
	235					240					245		
ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	779
Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	
			250					255					
TAC	AAG	CAT	CTT	GGG	ATT	GAA	TTT	ATG	GAG	GCG	GAG	GAG	818
Tyr	Lys	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ala	Glu	Glu	
260					265					270			
CTG	TAC	CAG	AAG	AGA	GTG	CTG	ACC	ATA	ACC	GGC	ATC	TGC	857
Leu	Tyr	Gln	Lys	Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	Cys	
		275					280					285	
ATC	GCC	CTC	CTT	GTG	GTC	GGC	ATC	ATG	TGT	GTG	GTG	GCC	896
Ile	Ala	Leu	Leu	Val	Val	Gly	Ile	Met	Cys	Val	Val	Ala	
				290					295				
TAC	TGC	AAA	ACC	AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	935
Tyr	Cys	Lys	Thr	Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	
	300					305					310		
CGT	CTT	CGG	CAG	AGC	CTT	CGG	TCT	GAA	CGA	AAC	AAT	ATG	974
Arg	Leu	Arg	Gln	Ser	Leu	Arg	Ser	Glu	Arg	Asn	Asn	Met	
			315					320					
ATG	AAC	ATT	GCC	AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	1013
Met	Asn	Ile	Ala	Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	
325					330					335			

FIG.2B

CCC	GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	1052
Pro	Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	
		340					345					350	
AAC	GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	1091
Asn	Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	
				355					360				
GAG	ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	1130
Glu	Thr	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	
	365					370					375		
CAT	CAC	TCC	ACT	ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	1169
His	His	Ser	Thr	Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	
			380					385					
TGG	AGC	AAC	GGA	CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	1208
Trp	Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	
390					395					400			
CAC	TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	1247
His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	
		405					410					415	
CAC	AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	1286
His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	
				420						425			
GGC	ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	1325
Gly	Thr	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	
	430					435					440		
CAT	GCC	AGA	GAA	ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	1364
His	Ala	Arg	Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	
			445					450					
CAT	AGT	GAA	AGG	TAT	GTG	TCA	GCC	ATG	ACC	ACC	CCG	GCT	1403
His	Ser	Glu	Arg	Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	
455					460					465			
CGT	ATG	TCA	CCT	GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	1442
Arg	Met	Ser	Pro	Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	
		470					475					480	
AAA	TCG	CCC	CCT	TCG	GAA	ATG	TCT	CCA	CCC	GTG	TCC	AGC	1481
Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	
				485					490				
ATG	ACG	GTG	TCC	ATG	CCT	TCC	ATG	GCG	GTC	AGC	CCC	TTC	1520
Met	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro	Phe	
	495					500					505		

FIG. 2C

ATG GAA GAA GAG AGA CCT CTA CTT CTC GTG ACA CCA CCA 1559
 Met Glu Glu Glu Arg Pro Leu Leu Val Thr Pro Pro
 510

AGG CTG CGG GAG AAG AAG TTT GAC CAT CAC CCT CAG CAG 1598
 Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln
 520 525 530

TTC AGC TCC TTC CAC CAC AAC CCC GCG CAT GAC AGT AAC 1637
 Phe Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn
 535 540 545

AGC CTC CCT GCT AGC CCC TTG AGG ATA GTG GAG GAT GAG 1676
 Ser Leu Pro Ala Ser Pro Leu Arg Ile Val Glu Asp Glu
 550 555

GAG TAT GAA ACG ACC CAA GAG TAC GAG CCA GCC CAA GAG 1715
 Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu
 560 565 570

CCT GTT AAG AAA CTC GCC AAT AGC CGG CGG GCC AAA AGA 1754
 Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala Lys Arg
 575 580

ACC AAG CCC AAT GGC CAC ATT GCT AAC AGA TTG GAA GTG 1793
 Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val
 585 590 595

GAC AGC AAC ACA AGC TCC CAG AGC AGT AAC TCA GAG AGT 1832
 Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser
 600 605 610

FIG.2D

GAA ACA GAA GAT GAA AGA GTA GGT GAA GAT ACG CCT TTC 1871
 Glu Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe
 615 620
 CTG GGC ATA CAG AAC CCC CTG GCA GCC AGT CTT GAG GCA 1910
 Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser Leu Glu Ala
 625 630 635
 ACA CCT GCC TTC CGC CTG GCT GAC AGC AGG ACT AAC CCA 1949
 Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg Thr Asn Pro
 640 645
 GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG 1988
 Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala Arg
 650 655 660
 CTG TCT AGT GTA ATT GCT AAC CAA GAC CCT ATT GCT GTA TA 2029
 Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val
 665 670 675
 A AACCTAAATA AACACATAGA TTCACCTGTA AAACTTTATT 2070
 TTATATAATA AAGTATTCCA CCTTAAATTA AACAAATTAT TTTATTTTAG 2120
 CAGTTCTGCA AATAGAAAAC AGGAAAAAAA CTTTATATAA TTAAATATAT 2170
 GTATGTAAAA ATGAAAAAAA AAAAAAAA 2199

FIG.2E

10/34

GTGGCTGCGG GGCAATTGAA AAAGAGCCGG CGAGGAGTTC CCCGAACTT 50

GTTGGAAGTC CGGGCTCGCG CGGAGGCCAG GAGCTGAGCG GCGGCGGCTG 100

CCGACGATG GGAGCGTGAG CAGGACGGTG ATAACCTCTC CCCGATCGGG 150

TTGCGAGGGC GCCGGGCAGA GGCCAGGACG CGAGCCGCCA GCGGCGGGAC 200

CCATCGACGA CTTCCCGGGG CGACAGGAGC AGCCCCGAGA GCCAGGGCGA 250

GCGCCCGTTC CAGGTGGCCG GACCGCCCGC CGCGTCCGCG CCGCGCTCCC 300

TGCAGGCAAC GGGAGACGCC CCCGCGCAGC GCGAGCGCCT CAGCGCGGCC 350

GCTCGCTCTC CCCATCGAGG GACAACTTT TCCCAAACCC GATCCGAGCC 400

CTTGACCAA ACTCGCCTGC GCCGAGAGCC GTCCGCGTAG AGCGCTCCGT 450

CTCCGGCGAG ATG TCC GAG CGC AAA GAA GGC AGA GGC AAA 490
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys
1 5 10

GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC GGC AAG AAG 529
Gly Lys Gly Lys Lys Lys Glu Arg Gly Ser Gly Lys Lys
15 20

CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA GCC TTG CCT 568
Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro
25 30 35

CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA 607
Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala
40 45

GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA 646
Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
50 55 60

TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG AAT GGG AAT 685
Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn
65 70 75

GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT ATC AAG ATA 724
Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile
80 85

FIG. 3A

CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC ATT AAC AAA 763
 Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys
 90 95 100

GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG 802
 Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
 105 110

ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC 841
 Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile
 115 120 125

ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT GGT ATG CCA 880
 Thr Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro
 130 135 140

GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA GAG TCT CCC 919
 Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu Ser Pro
 145 150

ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT ACT TCT 958
 Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn Thr Ser
 155 160 165

TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT 997
 Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu
 170 175

GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT 1036
 Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
 180 185 190

GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT TCA AAC CCC 1075
 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro
 195 200 205

TCG AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT 1114
 Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly
 210 215

GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAG 1153
 Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys
 220 225 230

GCG GAG GAG CTG TAC CAG AAG AGA GTG CTG ACC ATA ACC 1192
 Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr
 235 240

GGC ATC TGC ATC GCC CTC CTT GTG GTC GGC ATC ATG TGT 1231
 Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys
 245 250 255

GTG GTG GCC TAC TGC AAA ACC AAG AAA CAG CGG AAA AAG 1270
 Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys
 260 265 270

FIG. 3B

CTG CAT GAC CGT CTT CGG CAG AGC CTT CGG TCT GAA CGA 1309
 Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg
 275 280

AAC AAT ATG ATG AAC ATT GCC AAT GGG CCT CAC CAT CCT 1348
 Asn Asn Met Met Asn Ile Ala Asn Gly Pro His His Pro
 285 290 295

AAC CCA CCC CCC GAG AAT GTC CAG CTG GTG AAT CAA TAC 1387
 Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr
 300 305

GTA TCT AAA AAC GTC ATC TCC AGT GAG CAT ATT GTT GAG 1426
 Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu
 310 315 320

AGA GAA GCA GAG ACA TCC TTT TCC ACC AGT CAC TAT ACT 1465
 Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr
 325 330 335

TCC ACA GCC CAT CAC TCC ACT ACT GTC ACC CAG ACT CCT 1504
 Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro
 340 345

AGC CAC AGC TGG AGC AAC GGA CAC ACT GAA AGC ATC CTT 1543
 Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu
 350 355 360

TCC GAA AGC CAC TCT GTA ATC GTG ATG TCA TCC GTA GAA 1582
 Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu
 365 370

AAC AGT AGG CAC AGC AGC CCA ACT GGG GGC CCA AGA GGA 1621
 Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly
 375 380 385

CGT CTT AAT GGC ACA GGA GGC CCT CGT GAA TGT AAC AGC 1660
 Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser
 390 395 400

TTC CTC AGG CAT GCC AGA GAA ACC CCT GAT TCC TAC CGA 1699
 Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg
 405 410

GAC TCT CCT CAT AGT GAA AGG TAT GTG TCA GCC ATG ACC 1738
 Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr
 415 420 425

ACC CCG GCT CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA 1777
 Thr Pro Ala Arg Met Ser Pro Val Asp Phe His Thr Pro
 430 435

AGC TCC CCC AAA TCG CCC CCT TCG GAA ATG TCT CCA CCC 1816
 Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro
 440 445 450

FIG. 3C

GTG	TCC	AGC	ATG	ACG	GTG	TCC	AAG	CCT	TCC	ATG	GCG	GTC	1855
Val	Ser	Ser	Met	Thr	Val	Ser	Lys	Pro	Ser	Met	Ala	Val	
		455					460					465	
AGC	CCC	TTC	ATG	GAA	GAA	GAG	AGA	CCT	CTA	CTT	CTC	GTG	1894
Ser	Pro	Phe	Met	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	
				470					475				
ACA	CCA	CCA	AGG	CTG	CGG	GAG	AAG	AAG	TTT	GAC	CAT	CAC	1933
Thr	Pro	Pro	Arg	Leu	Arg	Glu	Lys	Lys	Phe	Asp	His	His	
	480					485					490		
CCT	CAG	CAG	TTC	AGC	TCC	TTC	CAC	CAC	AAC	CCC	GCG	CAT	1972
Pro	Gln	Gln	Phe	Ser	Ser	Phe	His	His	Asn	Pro	Ala	His	
			495					500					
GAC	AGT	AAC	AGC	CTC	CCT	GCT	AGC	CCC	TTG	AGG	ATA	GTG	2011
Asp	Ser	Asn	Ser	Leu	Pro	Ala	Ser	Pro	Leu	Arg	Ile	Val	
505					510					515			
GAG	GAT	GAG	GAG	TAT	GAA	ACG	ACC	CAA	GAG	TAC	GAG	CCA	2050
Glu	Asp	Glu	Glu	Tyr	Glu	Thr	Thr	Gln	Glu	Tyr	Glu	Pro	
		520					525					530	
GCC	CAA	GAG	CCT	GTT	AAG	AAA	CTC	GCC	AAT	AGC	CGG	CGG	2089
Ala	Gln	Glu	Pro	Val	Lys	Lys	Leu	Ala	Asn	Ser	Arg	Arg	
				535					540				
GCC	AAA	AGA	ACC	AAG	CCC	AAT	GGC	CAC	ATT	GCT	AAC	AGA	2128
Ala	Lys	Arg	Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	Asn	Arg	
	545					550					555		
TTG	GAA	GTG	GAC	AGC	AAC	ACA	AGC	TCC	CAG	AGC	AGT	AAC	2167
Leu	Glu	Val	Asp	Ser	Asn	Thr	Ser	Ser	Gln	Ser	Ser	Asn	
			560					565					
TCA	GAG	AGT	GAA	ACA	GAA	GAT	GAA	AGA	GTA	GGT	GAA	GAT	2206
Ser	Glu	Ser	Glu	Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	
570					575					580			
ACG	CCT	TTC	CTG	GGC	ATA	CAG	AAC	CCC	CTG	GCA	GCC	AGT	2245
Thr	Pro	Phe	Leu	Gly	Ile	Gln	Asn	Pro	Leu	Ala	Ala	Ser	
		585					590					595	
CTT	GAG	GCA	ACA	CCT	GCC	TTC	CGC	CTG	GCT	GAC	AGC	AGG	2284
Leu	Glu	Ala	Thr	Pro	Ala	Phe	Arg	Leu	Ala	Asp	Ser	Arg	
				600					605				
ACT	AAC	CCA	GCA	GGC	CGC	TTC	TCG	ACA	CAG	GAA	GAA	ATC	2323
Thr	Asn	Pro	Ala	Gly	Arg	Phe	Ser	Thr	Gln	Glu	Glu	Ile	
	610					615					620		
CAG	GCC	AGG	CTG	TCT	AGT	GTA	ATT	GCT	AAC	CAA	GAC	CCT	2362
Gln	Ala	Arg	Leu	Ser	Ser	Val	Ile	Ala	Asn	Gln	Asp	Pro	
			625					630					

FIG. 3D

ATT GCT GTA TAAACCTA AATAACACA TAGATTCACC TGTAACACTT 2410
 Ile Ala Val
 635 637

TATTTTATAT AATAAAGTAT TCCACCTTAA ATTAAACAAT TTATTTTATT 2460

TTAGCAGTTC TGCAAATAAA AAAAAAAAAA 2490

FIG. 3E

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GCGCCTGCCT CCAACCTGCG GCGGGGAGGT GGGTGGCTGC GGGGCAATTG 50

AAAAAGAGCC GCGGAGGAGT TCCCCGAAAC TTGTTGGAAC TCCGGGCTCG 100

CGCGGAGGCC AGGAGCTGAG CGGCGGCGGC TGCCGGACGA TGGGAGCGTG 150

AGCAGGACGG TGATAACCTC TCCCCGATCG GGTGCGAGG GCGCCGGGCA 200

GAGGCCAGGA CGCGAGCCGC CAGCGGCGGG ACCCATCGAC GACTTCCCGG 250

GGCGACAGGA GCAGCCCCGA GAGCCAGGGC GAGCGCCCGT TCCAGGTGGC 300

CGGACCGCCC GCCGCGTCCG CGCCGCGCTC CCTGCAGGCA ACGGGAGACG 350

CCCCCGCGCA GCGCGAGCGC CTCAGCGCGG CCGCTCGCTC TCCCCATCGA 400

GGGACAAACT TTTCCCAAAC CCGATCCGAG CCCTTGGACC AACTCGCCT 450

GCGCCGAGAG CCGTCCGCGT AGAGCGCTCC GTCTCCGGCG AG ATG 495
Met
1

TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 534
Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys
5 10

AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 573
Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala
15 20 25

GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 612
Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys
30 35 40

GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 651
Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
45 50

GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 690
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
55 60 65

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 729
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg
70 75

FIG. 4A

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AAA AAC AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA 768
Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro
80 85 90

GGG AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT 807
Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
95 100 105

GAT TCT GGA GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA 846
Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
110 115

GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG GAA 885
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu
120 125 130

TCA AAC GAG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA 924
Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
135 140

GGA GCA TAT GTG TCT TCA GAG TCT CCC ATT AGA ATA TCA 963
Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser
145 150 155

GTA TCC ACA GAA GGA GCA AAT ACT TCT TCA TCT ACA TCT 1002
Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser
160 165 170

ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG 1041
Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala
175 180

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1080
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
185 190 195

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG 1119
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
200 205

TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA 1158
Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
210 215 220

AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC 1197
Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
225 230 235

TTT CTG TCT CTG CCT GAA TAGGA GCATGCTCAG TTGGTGCTGC 1240
Phe Leu Ser Leu Pro Glu
240 241

TTTCTTGTTG CTGCATCTCC CCTCAGATTC CACCTAGAGC TAGATGTGTC 1290

FIG. 4B

TTACCAGATC TAATATTGAC TGCCTCTGCC TGTCGCATGA GAACATTAAC 1340
AAAAGCAATT GTATTACTTC CTCTGTTCGC GACTAGTTGG CTCTGAGATA 1390
CTAATAGGTG TGTGAGGCTC CGGATGTTTC TGGAATTGAT ATTGAATGAT 1440
GTGATACAAA TTGATAGTCA ATATCAAGCA GTGAAATATG ATAATAAAGG 1490
CATTTCAAAG TCTCACTTTT ATTGATAAAA TAAAAATCAT TCTACTGAAC 1540
AGTCCATCTT CTTTATACAA TGACCACATC CTGAAAAGGG TGTGCTAAG 1590
CTGTAACCGA TATGCACTTG AAATGATGGT AAGTTAATTT TGATTCAGAA 1640
TGTGTTATTT GTCACAAATA AACATAATAA AAGGAGTTCA GATGTTTTTC 1690
TTCATTAACC AAAAAAAAAA AAAAA 1715

FIG. 4C

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GAGGCGCCTG CCTCCAACCT GCGGGCGGGA GGTGGGTGGC TCGGGGGCAA 50

TTGAAAAAGA GCCGGCGAGG AGTTCCCCGA AACTTGTTGG AACTCCGGGC 100

TCGCGCGGAG GCCAGGAGCT GAGCGGCGGC GGCTGCCGGA CGATGGGAGC 150

GTGAGCAGGA CGGTGATAAC CTCTCCCCGA TCGGGTTGCG AGGGCGCCGG 200

GCAGAGGCCA GGACGCGAGC CGCCAGCGGC GGGACCCATC GACGACTTCC 250

CGGGGCGACA GGAGCAGCCC CGAGAGCCAG GGCGAGCGCC CGTTCCAGGT 300

GGCCGGACCG CCCGCCGCGT CCGCGCCGCG CTCCCTGCAG GCAACGGGAG 350

ACGCCCCCGC GCAGCGCGAG CGCCTCAGCG CGGCCGCTCG CTCTCCCCAT 400

CGAGGGACAA ACTTTTCCCA AACCCGATCC GAGCCCTTGG ACCAAACTCG 450

CCTGCGCCGA GAGCCGTCCG CGTAGAGCGC TCCGTCTCCG GCGAG AT 497
Met
1

G TCC GAG CGC AAA GAA GGC AGA GGC AAA GGG AAG GGC AAG 537
Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys
5 10

AAG AAG GAG CGA GGC TCC GGC AAG AAG CCG GAG TCC GCG 576
Lys Lys Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala
15 20 25

GCG GGC AGC CAG AGC CCA GCC TTG CCT CCC CAA TTG AAA 615
Ala Gly Ser Gln Ser Pro Ala Leu Pro Pro Gln Leu Lys
30 35 40

GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT TCC AAA CTA 654
Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
45 50

GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC 693
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
55 60 65

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA 732
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg
70 75

FIG. 5A

AAA AAC AAA CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA 771
 Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro
 80 85 90

GGG AAG TCA GAA CTT CGC ATT AAC AAA GCA TCA CTG GCT 810
 Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
 95 100 105

GAT TCT GGA GAG TAT ATG TGC AAA GTG ATC AGC AAA TTA 849
 Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
 110 115

GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG GAA 888
 Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu
 120 125 130

TCA AAC GAG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA 927
 Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 135 140

GGA GCA TAT GTG TCT TCA GAG TCT CCC ATT AGA ATA TCA 966
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser
 145 150 155

GTA TCC ACA GAA GGA GCA AAT ACT TCT TCA TCT ACA TCT 1005
 Val Ser Thr Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser
 160 165 170

ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA AAA TGT GCG 1044
 Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala
 175 180

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1083
 Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 185 190 195

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG 1122
 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 200 205

TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA 1161
 Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
 210 215 220

AAC TAC GTA ATG GCC AGC TTC TAC AAG GCG GAG GAG CTG 1200
 Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu
 225 230 235

TAC CAG AAG AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC 1239
 Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile
 240 245

GCC CTC CTT GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC 1278
 Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr
 250 255 260

FIG. 5B

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TGC	AAA	ACC	AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	CGT	1317
Cys	Lys	Thr	Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	Arg	
			265						270				
CTT	CGG	CAG	AGC	CTT	CGG	TCT	GAA	CGA	AAC	AAT	ATG	ATG	1356
Leu	Arg	Gln	Ser	Leu	Arg	Ser	Glu	Arg	Asn	Asn	Met	Met	
275						280					285		
AAC	ATT	GCC	AAT	GGG	CCT	CAC	CAT	CCT	AAC	CCA	CCC	CCC	1395
Asn	Ile	Ala	Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	Pro	
		290					295					300	
GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	AAC	1434
Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn	
				305					310				
GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG	1473
Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	
	315					320					325		
ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	1512
Thr	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	
			330					335					
CAC	TCC	ACT	ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	1551
His	Ser	Thr	Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	
340						345					350		
AGC	AAC	GGA	CAC	ACT	GAA	AGC	ATC	CTT	TCC	GAA	AGC	CAC	1590
Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Leu	Ser	Glu	Ser	His	
		355					360					365	
TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	CAC	1629
Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	His	
				370					375				
AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	GGC	1668
Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	
		380					385					390	
ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	1707
Thr	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	
			395					400					
GCC	AGA	GAA	ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	1746
Ala	Arg	Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	
405						410					415		
AGT	GAA	AGG	TAAAA	CCGAAGGCAA	AGCTACTGCA	GAGGAGAAAC	1790						
Ser	Glu	Arg											
			420										

FIG.5C

TCAGTCAGAG AATCCCTGTG AGCACCTGCG GTCTCACCTC AGGAAATCTA 1840
CTCTAATCAG AATAAGGGGC GGCAGTTACC TGTTC TAGGA GTGCTCCTAG 1890
TTGATGAAGT CATCTCTTTG TTTGACGGAA CTTATTTCTT CTGAGCTTCT 1940
CTCGTCGTCC CAGTGA CTGA CAGGCAACAG ACTCTTAAAG AGCTGGGATG 1990
CTTTGATGCG GAAGGTGCAG CACATGGAGT TTCCAGCTCT GGCCATGGGC 2040
TCAGACCCAC TCGGGGTCTC AGTGTCTCTA GTTGTAACAT TAGAGAGATG 2090
GCATCAATGC TTGATAAGGA CCCTTCTATA ATTCCAATTG CCAGTTATCC 2140
AAACTCTGAT TCGGTGGTCG AGCTGGCCTC GTGTTCTTAT CTGCTAACCC 2190
TGTCTTACCT TCCAGCCTCA GTTAAGTCAA ATCAAGGGCT ATGTCATTGC 2240
TGAATGTCAT GGGGGGCAAC TGCTTGCCCT CCACCCTATA GTATCTATTT 2290
TATGAAATTC CAAGAAGGGA TGAATAAATA AATCTCTTGG ATGCTGCGTC 2340
TGGCAGTCTT CACGGGTGGT TTTCAAAGCA GAAAAAAAAA AAAAAAAAAA 2390
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 2431

FIG. 5D

16	1	MSERKEGRGKGKGKKKERGS	GKKPES	AAGSQSPAL	PPRL	KEMKSQES	AAG		
11	1	MSERKEGRGKGKGKKKERGS	GKKPES	AAGSQSPAL	PPQL	KEMKSQES	AAG		
76	1	MSERKEGRGKGKGKKKERGS	GKKPES	AAGSQSPAL	PPQL	KEMKSQES	AAG		
84	1	MSERKEGRGKGKGKKKERGS	GKKPES	AAGSQSPAL	PPQL	KEMKSQES	AAG		
78	1	MSERKEGRGKGKGKKKERGS	GKKPES	AAGSQSPAL	PPQL	KEMKSQES	AAG		
16	51	SKLVLRCE	TSSEYSSL	RFKWF	KNGNEL	NRKKNK	QNIKI QKKPGKSEL	RIN	
11	51	SKLVLRCE	TSSEYSSL	RFKWF	KNGNEL	NRKKNK	QNIKI QKKPGKSEL	RIN	
76	51	SKLVLRCE	TSSEYSSL	RFKWF	KNGNEL	NRKKNK	QNIKI QKKPGKSEL	RIN	
84	51	SKLVLRCE	TSSEYSSL	RFKWF	KNGNEL	NRKKNK	QNIKI QKKPGKSEL	RIN	
78	51	SKLVLRCE	TSSEYSSL	RFKWF	KNGNEL	NRKKNK	QNIKI QKKPGKSEL	RIN	
16	101	KASLADSGEY	MCKVIS	SKLGND	SASANI	TIVES	NEIITGMPASTE	GAYVSS	
11	101	KASLADSGEY	MCKVIS	SKLGND	SASANI	TIVES	NEIITGMPASTE	GAYVSS	
76	101	KASLADSGEY	MCKVIS	SKLGND	SASANI	TIVES	NEIITGMPASTE	GAYVSS	
84	101	KASLADSGEY	MCKVIS	SKLGND	SASANI	TIVES	NEIITGMPASTE	GAYVSS	
78	101	KASLADSGEY	MCKVIS	SKLGND	SASANI	TIVES	NEIITGMPASTE	GAYVSS	
16	151	ESPIRISV	STEGANT	SSST	STST	TGTSHL	VKCAEKE	KTF CVN GGECF	MVK
11	151	ESPIRISV	STEGANT	SSST	STST	TGTSHL	VKCAEKE	KTF CVN GGECF	MVK
76	151	ESPIRISV	STEGANT	SSST	STST	TGTSHL	VKCAEKE	KTF CVN GGECF	MVK
84	151	ESPIRISV	STEGANT	SSST	STST	TGTSHL	VKCAEKE	KTF CVN GGECF	MVK
78	151	ESPIRISV	STEGANT	SSST	STST	TGTSHL	VKCAEKE	KTF CVN GGECF	MVK

FIG. 6A

16	201	DL	SN	PS	RY	L	CK	C	Q	P	G	F	T	G	A	R	C	T	E	N	V	P	M	K	V	Q	N	Q	-	-	-	-	E	K	A	E	E	L	Y	Q	K	R	V	L	T						
11	201	DL	SN	PS	RY	L	CK	C	P	N	E	F	T	G	D	R	C	Q	N	Y	V	M	A	S	F	Y	K	H	L	G	I	E	F	M	E	A	E	E	L	Y	Q	K	R	V	L	T					
76	201	DL	SN	PS	RY	L	CK	C	P	N	E	F	T	G	D	R	C	Q	N	Y	V	M	A	S	F	Y	K	-	-	-	-	-	-	-	-	-	A	E	E	L	Y	Q	K	R	V	L	T				
84	201	DL	SN	PS	RY	L	CK	C	P	N	E	F	T	G	D	R	C	Q	N	Y	V	M	A	S	F	Y	K	-	-	-	-	-	-	-	-	-	A	E	E	L	Y	Q	K	R	V	L	T				
78	201	DL	SN	PS	RY	L	CK	C	P	N	E	F	T	G	D	R	C	Q	N	Y	V	M	A	S	F	Y	S	T	S	T	P	F	L	S	L	P	E														
16	246	IT	G	I	C	I	A	L	L	V	V	G	I	M	C	V	V	A	Y	C	K	T	K	K	Q	R	K	K	L	H	D	R	L	R	Q	S	L	R	S	E	R	N	N	M	M	N	I	A	N	G	
11	251	IT	G	I	C	I	A	L	L	V	V	G	I	M	C	V	V	A	Y	C	K	T	K	K	Q	R	K	K	L	H	D	R	L	R	Q	S	L	R	S	E	R	N	N	M	M	N	I	A	N	G	
76	243	IT	G	I	C	I	A	L	L	V	V	G	I	M	C	V	V	A	Y	C	K	T	K	K	Q	R	K	K	L	H	D	R	L	R	Q	S	L	R	S	E	R	N	N	M	M	N	I	A	N	G	
84	243	IT	G	I	C	I	A	L	L	V	V	G	I	M	C	V	V	A	Y	C	K	T	K	K	Q	R	K	K	L	H	D	R	L	R	Q	S	L	R	S	E	R	N	N	M	M	N	I	A	N	G	
16	296	P	H	H	P	N	P	P	P	E	N	V	Q	L	V	N	Q	Y	V	S	K	N	V	I	S	S	E	H	I	V	E	R	E	A	E	T	S	F	S	T	S	H	Y	T	S	T	A	H	H	S	T
11	301	P	H	H	P	N	P	P	P	E	N	V	Q	L	V	N	Q	Y	V	S	K	N	V	I	S	S	E	H	I	V	E	R	E	A	E	T	S	F	S	T	S	H	Y	T	S	T	A	H	H	S	T
76	293	P	H	H	P	N	P	P	P	E	N	V	Q	L	V	N	Q	Y	V	S	K	N	V	I	S	S	E	H	I	V	E	R	E	A	E	T	S	F	S	T	S	H	Y	T	S	T	A	H	H	S	T
84	293	P	H	H	P	N	P	P	P	E	N	V	Q	L	V	N	Q	Y	V	S	K	N	V	I	S	S	E	H	I	V	E	R	E	A	E	T	S	F	S	T	S	H	Y	T	S	T	A	H	H	S	T
16	346	T	V	T	Q	T	P	S	H	S	W	S	N	G	H	T	E	S	I	L	S	E	S	H	S	V	I	V	M	S	S	V	E	N	S	R	H	S	S	P	T	G	G	P	R	G	R	L	N	G	T
11	351	T	V	T	Q	T	P	S	H	S	W	S	N	G	H	T	E	S	I	L	S	E	S	H	S	V	I	V	M	S	S	V	E	N	S	R	H	S	S	P	T	G	G	P	R	G	R	L	N	G	T
76	343	T	V	T	Q	T	P	S	H	S	W	S	N	G	H	T	E	S	I	L	S	E	S	H	S	V	I	V	M	S	S	V	E	N	S	R	H	S	S	P	T	G	G	P	R	G	R	L	N	G	T
84	343	T	V	T	Q	T	P	S	H	S	W	S	N	G	H	T	E	S	I	L	S	E	S	H	S	V	I	V	M	S	S	V	E	N	S	R	H	S	S	P	T	G	G	P	R	G	R	L	N	G	T

FIG. 6B

16	396	GGPRECNSFLRHARETPD	SYRDS	PHSERYVS	AMTT	P	ARMSP	VDFHT	PSSSP
11	401	GGPRECNSFLRHARETPD	SYRDS	PHSERYVS	AMTT	P	ARMSP	VDFHT	PSSSP
76	393	GGPRECNSFLRHARETPD	SYRDS	PHSERYVS	AMTT	P	ARMSP	VDFHT	PSSSP
84	393	GGPRECNSFLRHARETPD	SYRDS	PHSER	-----				
16	446	KSPPEMSPPVSSMT	VSMPS	MAVSP	MEERPL	LLV	TPPRL	REKKF	DHHP
11	451	KSPPEMSPPVSSMT	VSMPS	MAVSP	MEERPL	LLV	TPPRL	REKKF	DHHP
76	443	KSPPEMSPPVSSMT	VSKP	SMAVSP	MEERPL	LLV	TPPRL	REKKF	DHHP
16	496	QQFSSFHHNPAHDS	NSLPA	SPLR	IVED	EEYETT	QEYEP	AQEP	VKKLANSR
11	501	QQFSSFHHNPAHDS	NSLPA	SPLR	IVED	EEYETT	QEYEP	AQEP	VKKLANSR
76	493	QQFSSFHHNPAHDS	NSLPA	SPLR	IVED	EEYETT	QEYEP	AQEP	VKKLANSR
16	546	RAKRTKPNGHIANR	LEVDS	NTSSQ	SSNSE	SETE	DERV	GEDT	PFLGIQNPL
11	551	RAKRTKPNGHIANR	LEVDS	NTSSQ	SSNSE	SETE	DERV	GEDT	PFLGIQNPL
76	543	RAKRTKPNGHIANR	LEVDS	NTSSQ	SSNSE	SETE	DERV	GEDT	PFLGIQNPL
16	596	AASLEATPAFRLA	DSRTNP	AGR	FSTQ	EEIQ	-----		
11	601	AASLEATPAFRLA	DSRTNP	AGR	FSTQ	EEIQ	ARLSSV	IANQD	PIAV
76	593	AASLEATPAFRLA	DSRTNP	AGR	FSTQ	EEIQ	ARLSSV	IANQD	PIAV

FIG. 6C

1 GGGTACCATGGGTGCGGTGAGCGCGTTTCCCGCCTGAGCGCAACTAGCGGC
 51 GGGTCGTGGGCACCTCCAGAAAAGATCCCGCACCATCCTCCAGGATCCAA
 101 TGGCCTTGGAGAGAGGGCTGCAGGGCCCGGACATTGCTGACTCTTCAG
 151 AACGTGCTGACATGGAGCCAGGTAGACTGAAATTATCATGTGTCCAAATT
 201 AAAATTGCATACTTCAAGGATTATTTGAAGGACTATTCTTAGACCCCTTTT
 251 AAGAAGATTTAAAGAAAAACCACTCGGCCCTGAGTGCGGCGAGGACCCTG

 301 TTTGTGGATGTGGAGGAGCGCGGGCCGGAGGCCATGGACGTGAAGGAGAG
 1 M D V K E R

 351 GAAGCCTTACCGCTCGCTGACCCGCGCGCCGCGACGCCGAGCGCCGCTACA
 7 K P Y R S L T R R R D A E R R Y T

 401 CCAGCTCGTCCGCGGACAGCGAGGAGGGCAAAGCCCCGCAGAAATCGTAC
 24 S S S A D S E E G K A P Q K S Y

 451 AGCTCCAGCGAGACCCTGAAGGCCTACGACCAGGACGCCCGCCTAGCCTA
 40 S S S E T L K A Y D Q D A R L A Y

 501 TGGCAGCCGCGTCAAGGACATTGTGCCGACGAGGCGCGAGGAATTCTGCC
 57 G S R V K D I V P Q E A E E F C R

 551 GCACAGGTGCCAACTTCACCCTGCGGGAGCTGGGGCTGGAAGAAGTAACG
 74 T G A N F T L R E L G L E E V T

 601 CCCCCTCACGGGACCCTGTACCGGACAGACATTGGCCTCCCCCACTGCGG
 90 P P H G T L Y R T D I G L P H C G

 651 CTA CTCCATGGGGGCTGGCTCTGATGCCGACATGGAGGCTGACACGGTGC
 107 Y S M G A G S D A D M E A D T V L

 701 TGTCCCCTGAGCACCCCGTGCGTCTGTGGGGCCGGAGCACACGGTCAGGG
 124 S P E H P V R L W G R S T R S G

 751 CGCAGCTCCTGCCTGTCCAGCCGGGCCAATTCCAATCTCACACTCACCGA
 140 R S S C L S S R A N S N L T L T D

 801 CACCGAGCATGAAAACACTGAGACTGATCATCCGGGCGGCCTGCAGAACC
 157 T E H E N T E T D H P G G L Q N H

 851 ACGCGCGGCTCCGGACGCCGCCGCCGCTCTCGCACGCCACACCCCC
 174 A R L R T P P P P L S H A H T P

 901 AACCAGCACCACGCGGCCTCCATTA ACTCCCTGAACCGGGGCAACTTCAC
 190 N Q H H A A S I N S L N R G N F T

 951 GCCGAGGAGCAACCCAGCCCGGCCCCACGGACCACTCGCTCTCCGGAG
 207 P R S N P S P A P T D H S L S G E

 1001 AGCCCCCTGCCGGCGGCGCCAGGAGCCTGCCACGCCAGGAGAACTGG
 224 P P A G G A Q E P A H A Q E N W

 1051 CTGCTCAACAGCAACATCCCCCTGGAGACCAGAAACCTAGGCAAGCAGCC
 240 L L N S N I P L E T R N L G K Q P

FIG. 7A

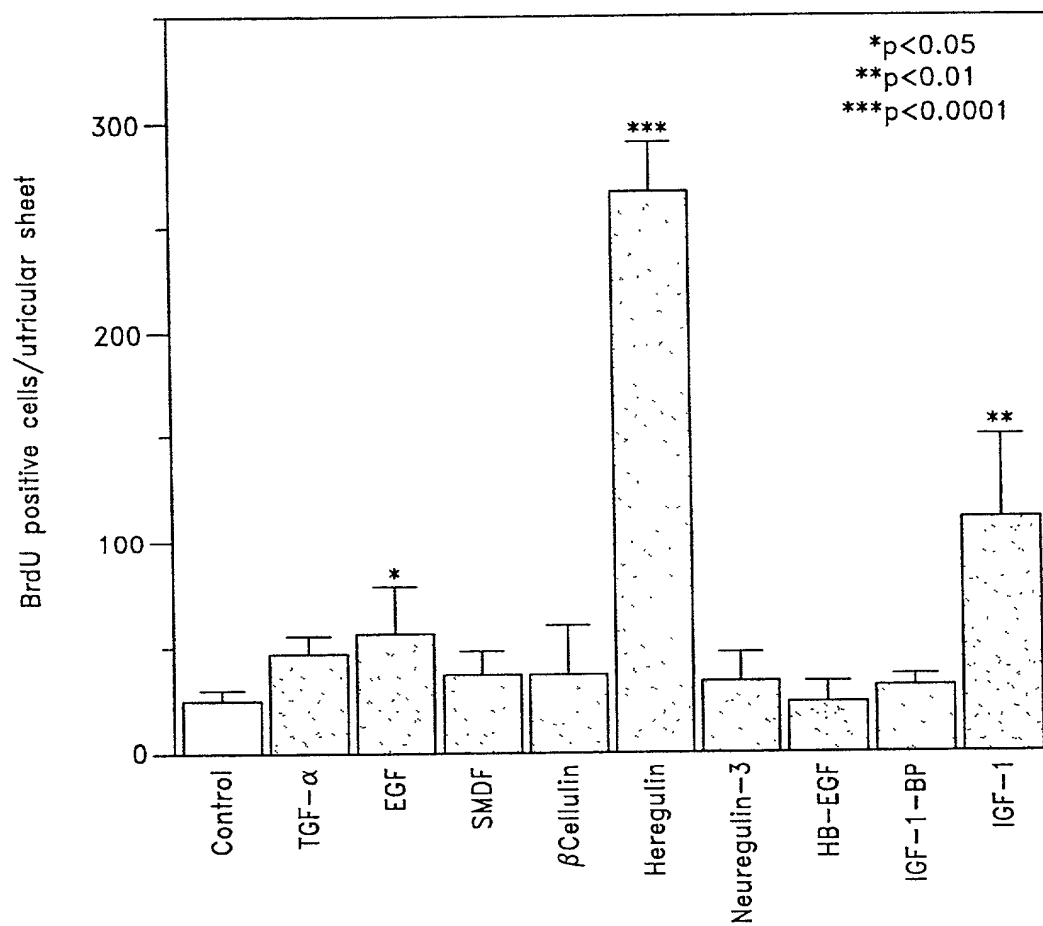
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 557 T T A I A L P P R L K E M K S Q E
 2051 AATCGGCTGCAGGTTCCAAACTAGTCCTTCGGTGTGAAACCAGTTCTGAA
 574 S A A G S K L V L R C E T S S E
 2101 TACTCCTCTCTCAGATTCAAGTGGTTCAAGAATGGGAATGAATTGAATCG
 590 Y S S L R F K W F K N G N E L N R
 2151 AAAAAACAAACCACAAAATATCAAGATACAAAAAAGCCAGGGAAGTCAG
 607 K N K P Q N I K I Q K K P G K S E
 2201 AACTTCGCATTAAACAAAGCATCACTGGCTGATTCTGGAGAGTATATGTGC
 624 L R I N K A S L A D S G E Y M C
 2251 AAAGTGATCAGCAAATTAGGAAATGACAGTGCCTCTGCCAATATCACCAT
 640 K V I S K L G N D S A S A N I T I
 2301 CGTGAATCAAACGAGATCATCACTGGTATGCCAGCCTCAACTGAAGGAG
 657 V E S N E I I T G M P A S T E G A
 2351 CATATGTGTCTTCAGAGTCTCCATTAGAATATCAGTATCCACAGAAGGA
 674 Y V S S E S P I R I S V S T E G
 2401 GCAAATACTTCTTCATCTACATCTACATCCACCACTGGGACAAGCCATCT
 690 A N T S S S T S T S T T G T S H L
 2451 TGTAATAATGTGCGGAGAAGGAGAAAACCTTCTGTGTGAATGGAGGGGAGT
 707 V K (C) A E K E K T F (C) V N G G E (C)
 2501 GCTTCATGGTGAAAGACCTTTCAAACCCCTCGAGATACTTGTGCAAGTGC
 724 F M V K D L S N P S R Y L (C) K (C)
 2551 CCAAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGGCCAGCTT
 740 P N E F T G D R (C) Q N Y V M A S F
 2601 CTACAGTACGTCCACTCCCTTTCTGTCTCTGCCTGAATAGGAGCATGCTC
 757 Y S T S T P F L S L P E
 2651 AGTTGGTGCTGCTTTCTTGTTGCTGCATCTCCCCTCAGATTCCACCTAGA
 2701 GCTAGATGTGTCTTACCAGATCTAATATTGACTGCCTCTGCCTGTGCGCAT
 2751 GAGAACATTAACAAAAGCAATTGTATTACTTCCTCTGTTCGCGACTAGTT
 2801 GGCTCTGAGATACTAATAGGTGTGTGAGGCTCCGGATGTTTCTGGAATTG
 2851 ATATTGAATGATGTGATACAAATTGATAGTCAATATCAAGCAGTGAAATA
 2901 TGATAATAAAGGCATTTCAAAGTCTCACTTTTATTGATAAAATAAAAATC
 2951 ATTCTACTGAACAGTCCATCTTCTTTATACAATGACCACATCCTGAAAAG
 3001 GGTGTTGCTAAGCTGTAACCGATATGCACTTGAAATGATGGTAAGTTAAT
 3051 TTTGATTCAGAATGTGTTATTTGTACAAATAAACATAATAAAAGGAAAA
 3101 AAAAAAAAAA

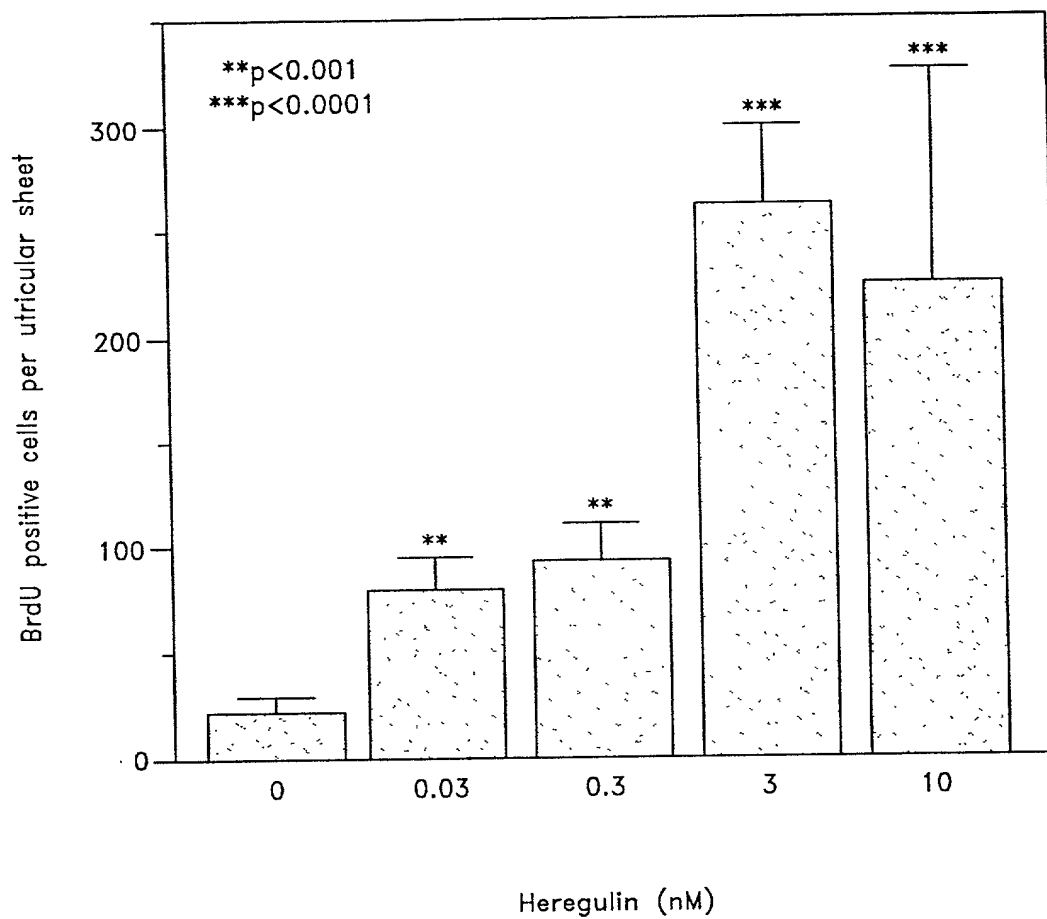
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 257 F L G T L Q D N L I E M D I L G A
 1151 CCTCCCGCCATGATGGGGCTTACAGTGACGGGCACTTCTCTTCAAGCCT
 274 S R H D G A Y S D G H F L F K P
 1201 GGAGGCACCTCCCCGCTCTTCTGCACCACATCACCAGGGTACCCACTGAC
 290 G G T S P L F C T T S P G Y P L T
 1251 GTCCAGCACAGTGTACTCTCCTCCGCCCCGACCCCTGCCCCGCAGCACCT
 307 S S T V Y S P P P R P L P R S T F
 1301 TCGCCCGGCGGGCCTTTAACCTCAAGAAGCCCTCCAAGTACTGTAAGTGG
 324 A R P A F N L K K P S K Y C N W
 1351 AAGTGCGCAGCCCTGAGCGCCATCGTCATCTCAGCCACTCTGGTCATCCT
 340 K C A A L S A I V I S A T L V I L
 1401 GCTGGCATACTTTGTGGCCATGCACCTGTTTGGCCTAAACTGGCACCTGC
 357 L A Y F V A M H L F G L N W H L Q
 1451 AGCCGATGGAGGGGCGAGATGTATGAGATCACGGAGGACACAGCCAGCAGT
 374 P M E G Q M Y E I T E D T A S S
 1501 TGGCCTGTGCCAACCGACGTCTCCCTATACCCCTCAGGGGGCACTGGCTT
 390 W P V P T D V S L Y P S G G T G L
 1551 AGAGACCCCTGACAGGAAAGGCAAAGGAACCACAGAAGGAAAGCCAGTA
 407 E T P D R K G K G T T E G K P S S
 1601 GTTCTTTTCCAGAGGACAGTTTCATAGATTCTGGAGAAATTGATGTGGGA
 424 F F P E D S F I D S G E I D V G
 1651 AGGCGAGCTTCCCAGAAGATTCTCCTGGCACTTTCTGGAGATCTCAAGT
 440 R R A S Q K I P P G T F W R S Q V
 1701 GTTCATAGACCATCCTGTGCATCTGAAATTCAATGTGTCTCTGGGAAAGG
 457 F I D H P V H L K F N V S L G K A
 1751 CAGCCCTGGTTGGCATTATGGCAGAAAAGGCCTCCCTCCTTCACATACA
 474 A L V G I Y G R K G L P P S H T
 1801 CAGTTTGACTTTGTGGAGCTGCTGGATGGCAGGAGGCTCCTAACCAGGA
 490 Q F D F V E L L D G R R L L T Q E
 1851 GGCGCGGAGCCTAGAGGGGACCCGCGCCAGTCTCGGGGAACTGTGCCCC
 507 A R S L E G T P R Q S R G T V P P
 1901 CCTCCAGCCATGAGACAGGCTTCATCCAGTATTTGGATTGAGGAATCTGG
 524 S S H E T G F I Q Y L D S G I W
 1951 CACTTGGCTTTTTTACAATGACGGAAAGGAGTCAGAAGTGGTTTCCTTTCT
 540 H L A F Y N D G K E S E V V S F L

1 GAATTCGGGACAGCCTCTCCTGCCGCCGCTGCTGCTGCCGCCGCCGCCACCGCCGGCTGGTCTCTCTGCTTT
 76 TACTTCTCCTGCATGACAGTTGTTTTCTTTCATCTGAGCAGACACCAGCTTCAGATGCTCGAGGTGAGAAACATGC
 151 CTTTCAGTTTGGGCTACTGGTTTACTTAATTAATCAGCCGGCAGCTCCGTCGATCTATTTTCGTCCCTGTCTCT
 226 TGACGAGCCCCGGATGGTTTGGAGTAGCATTAAAAAGAACTAGAAAAAGTGGCCAGAAACAGCAGCTTAAAGAAT
 301 TATTACGATATACTTTGATTTTGTAGTTGCTAGGAGCTTTTCTTCCCCCTTGCATCTTTCTGAACTCTTCTTGA
 376 TTTTAATAATGGCCTTGGACTTGGACGATTATCGATTTCCCCCTGTAAGATGCTGTATCATTGGTTGGGGGGG
 451 CCTCTGCGTGGTAATGGACCGTGAGAGCGGCCAGGCCTTCTTCTGAGAGGTGAGCCGATGGAGATTTATCCCCAG
 1 M E I Y S P D
 526 ACATGTCTGAGGTGCGCCGCCGAGAGGTCTCCAGCCCTCCACTCAGCTGAGTGCAGACCCATCTCTTGATGGGC
 8 M S E V A A E R S S S P S T Q L S A D P S L D G L
 601 TTCCGGCAGCAGAAGACATGCCAGAGCCCCAGACTGAAGATGGGAGAACCCCTGGACTCGTGGGCCTGGCCGTGC
 33 P A A E D M P E P Q T E D G R T P G L V G L A V P
 676 CCTGCTGTGCGTGCTTAGAAGCTGAGCGCCTGAGAGGTTGCCTCAACTCAGAGAAAATCTGCATTGTCCCCATCC
 58 [C] [C] A [C] L E A E R L R G [C] L N S E K I [C] I V P I L
 751 TGGCTTGCCTGGTCAGCCTCTGCCTCTGCATCGCCGGCCTCAAGTGGGTATTTGTGACAAGATCTTTGAATATG
 83 A [C] L V S L [C] L [C] I A G L K W V F V D K I F E Y D
 826 ACTCTCCTACTCACCTTGACCCTGGGGGGTTAGGCCAGGACCTATTATTTCTCTGGACGCAACTGCTGCCTCAG
 108 S P T H L D P G G L G Q D P I I S L D A T A A S A
 901 CTGTGTGGGTGTCGTCTGAGGCATACACTTCACCTGTCTCTAGGGCTCAATCTGAAAGTGAGGTTCAAGTTACAG
 133 V W V S S E A Y T S P V S R A Q S E S E V Q V T V
 976 TGCAAGGTGACAAGGCTGTTGTCTCCTTTGAACCATCAGCGGCACCGACACCGAAGAATCGTATTTTGCCTMTT
 158 Q G D K A V V S F E P S A A P T P K N R I F A F S
 1051 CTTTCTTGCCG1CCACTGCGCCATCCTTCCCTTCAACCCACCCGGAACCTGAGGTGAGAACGCCCAAGTCAGCAA
 183 F L P S T A P S F P S P T R N P E V R T P K S A T
 1126 CTCAGCCACAAACAACAGAACTAATCTCCAACTGCTCCTAACTTTCTACATCTACATCCACCACTGGGACAA
 208 Q P Q T T E T N L Q T A P K L S T S T S T T G T S
 1201 GCCATCTTGTAATAATGTGCGGAGAAGGAGAAAACTTTCTGTGTGAATGGAGGGGAGTGCTTCATGGTGAAAGACC
 233 H L V K [C] A E K E K T F [C] V N G G E [C] F M V K D L
 1276 TTTCAAACCCCTCGAGATACTTGTGCAAGTGCCCAATGAGTTTACTGGTGATCGCTGCCAAAACCTACGTAATGG
 258 S N P S R Y L [C] K [C] P N E F T G D R [C] Q N Y V M A
 1351 CCAGCTTCTACAGTACGTCCACTCCCTTTCTGTCTCTGCCTGAATAGGAGCATGCTCAGTTGGTGTGCTTTCTT
 283 S F Y S T S T P F L S L P E O
 1426 GTTGCTGCATCTCCCCTCAGATTCCACCTAGAGCTAGATGTGTCTTACCAGATCTAATATTGACTGCCTCTGCCT
 1501 GTCGCATGAGAACATTAACAAAAGCAATTGTATTACTTCTCTGTTCGCGACTAGTTGGCTCTGAGATACTAATA
 1576 GGTGTGTGAGGCTCCGGATGTTTCTGGAATTGATATTGAATGATGTGATACAAATTGATAGTCAATATCAAGCAG
 1651 TGAAATATGATAATAAAGGCATTTCAAAGTCTCACTTTTATTGATAAAATAAAAATCATTCTACTGAACAGTCCA
 1726 TCTTCTTTATACAATGACCACATCCTGAAAAGGTGTTGCTAAGCTGTAACCGATATGCACTTGAAATGATGGTA
 1801 AGTTAATTTTGATTGAGAAATGTGTTATTGTGCAAAATAAACATAATAAAAGGAAAAAAAAAACCCGAATTC

EGF
-like

FIG. 8

*FIG. 9*

*FIG. 10*

Heregulin increases the number of 3H-thymidine labeled cells in supporting and hair cell layers in gentamicin-treated utricles

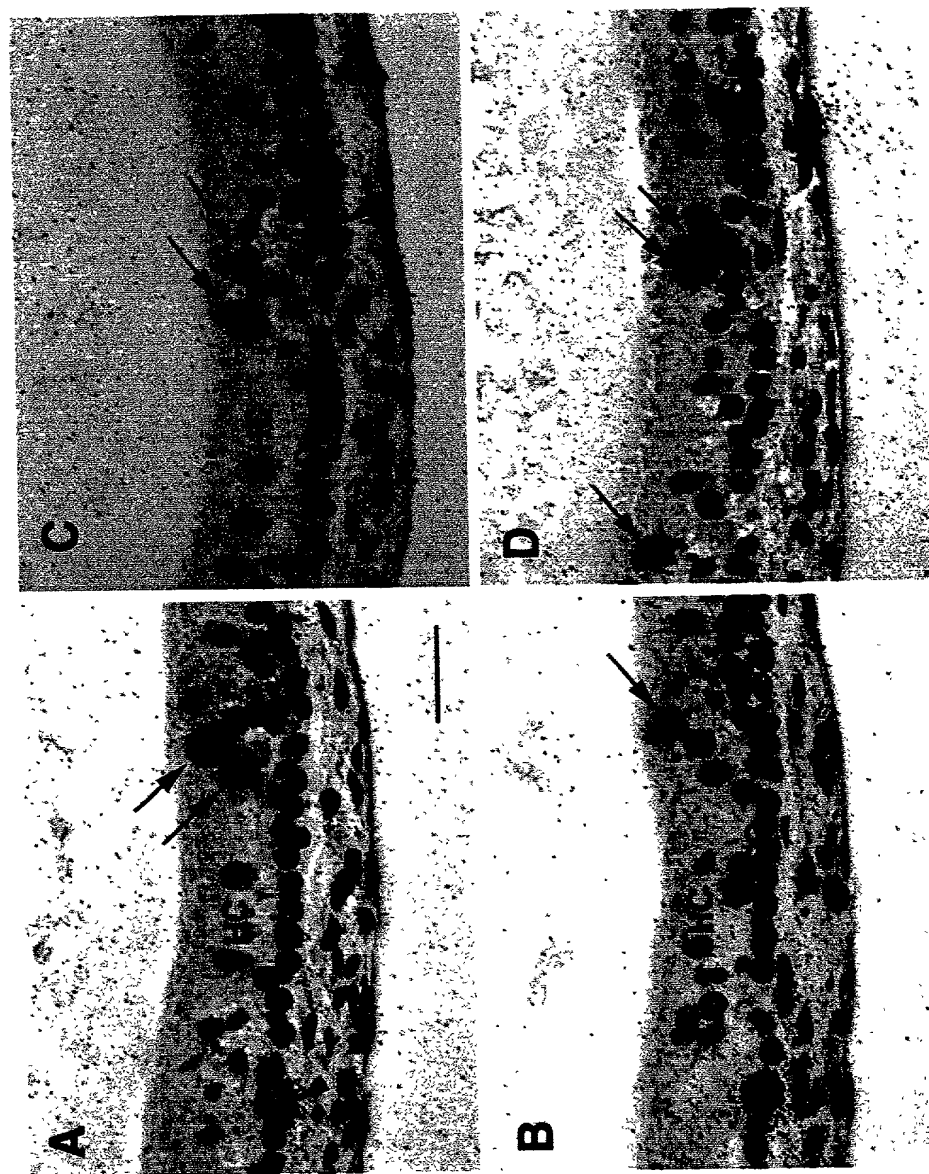


FIG. 11

Heregulin Enhances the Numbers of ^3H -thymidine Labeled Cells in Both Supporting and Hair Cell Layers

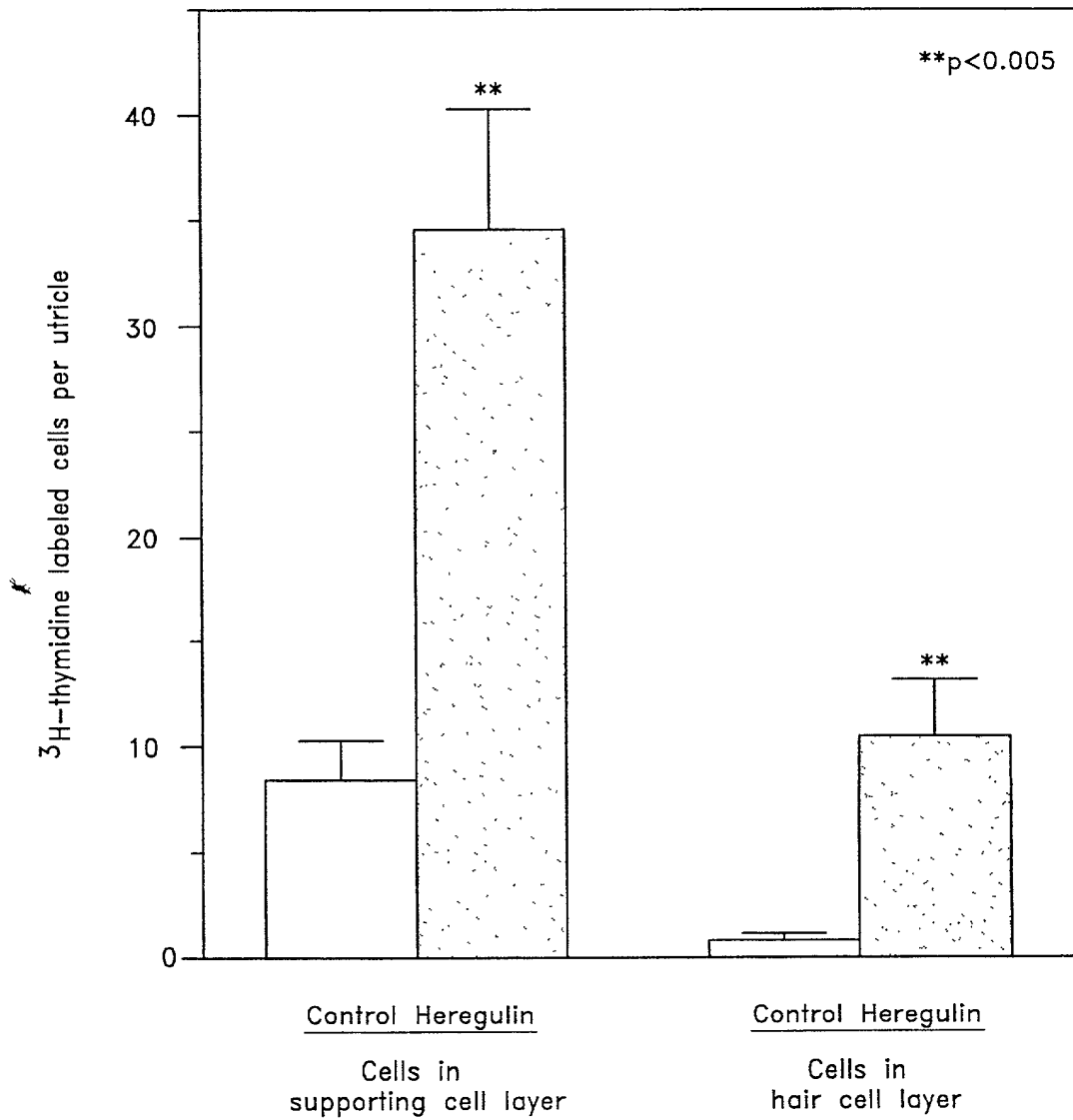
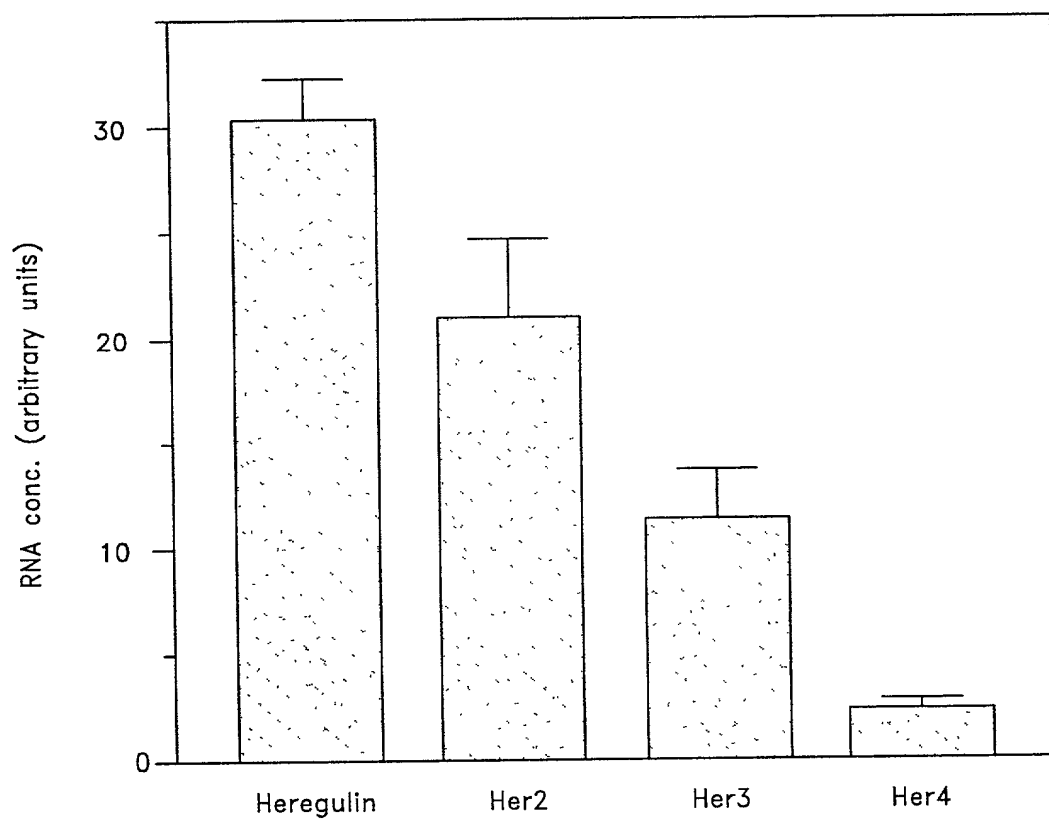


FIG. 12

*FIG. 13*

HER-2 Immunostaining

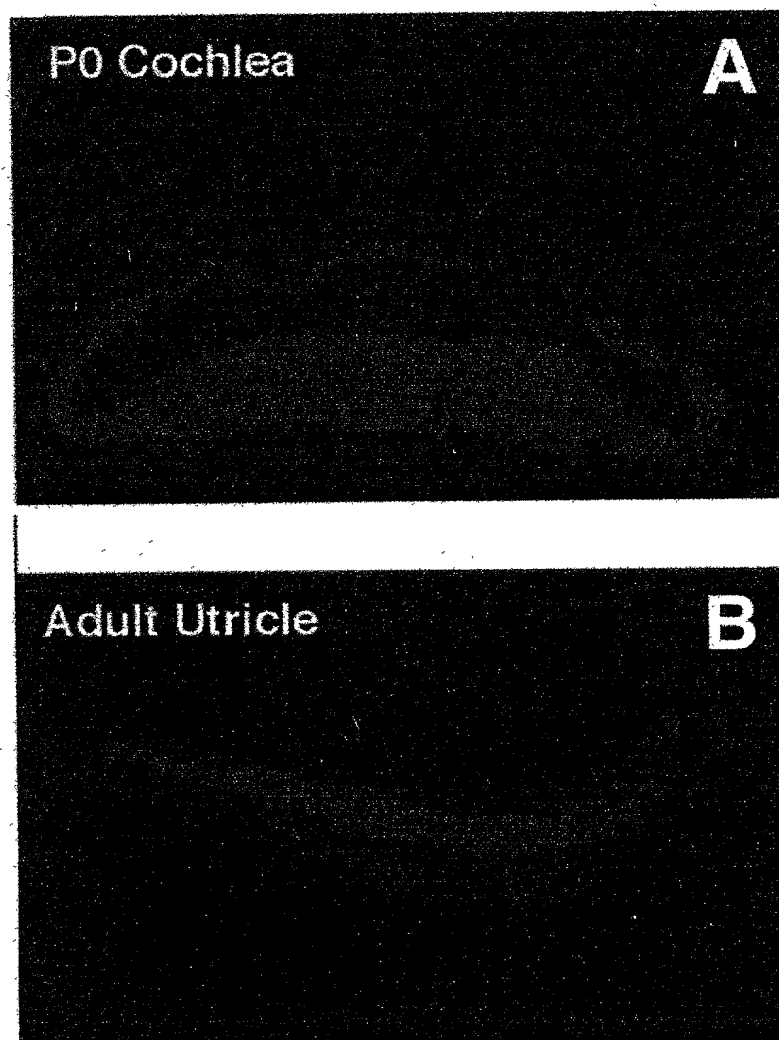


FIG.14